

A STOCHASTIC EPIDEMIC MODEL OF THE COVID19 DISEASE DATA FROM MEXICO

Brandon Iván Méndez-Barrera¹, Ponciano Jorge Escamilla-Ambrosio², Abraham Rodríguez-Mota³
Instituto Politécnico Nacional, Centro de Investigación en Computación.

Av. Juan de Dios Bátiz S/N, Nueva Industrial Vallejo, Gustavo A. Madero, 07738, Mexico.

Cel. 15561882582, 25530592860

¹bmendezb1200@alumno.ipn.mx, ²pescamilla@cic.ipn.mx, ³arodrigm@cic.ipn.mx

RESUMEN.

En este trabajo se presenta un modelo del comportamiento de la enfermedad por coronavirus (COVID-19) en México, utilizando una Cadena de Markov discreta. Este modelo considera varias fases de la enfermedad que una persona puede experimentar durante el periodo de infección como parte de un estado establecido en un modelo de cadena de Markov, (los estados son susceptibles, infectados, asintomáticos, sintomáticos, personas críticas como hospitalizados y cuidados intensivos, fallecidos y recuperados), considerando las probabilidades de transitar de un estado a otro (por ejemplo, la probabilidad de estar infectado, probabilidad de recuperarse de una enfermedad, etc.) y también incluye un gráfico para mostrar las posibles vías en el curso de la enfermedad. Los datos de México con fecha 10 de junio de 2020 se utilizaron para construir el modelo presentado. Este trabajo incluye un gráfico donde se muestra el comportamiento de contagio de una persona infectada (sintomática y asintomática) sobre personas susceptibles, este material gráfico del modelo está desarrollado con herramientas Python, para una mejor representación de la información gráfica y visual.

Palabras clave: espacio de estados, matriz de probabilidad, gráfico modelo, probabilidades de transición.

ABSTRACT.

In this work, a model of the behavior of the coronavirus disease (COVID-19) in Mexico, using a discrete Markov Chain, is presented. This model considers several phases of the disease that a person can experiment during the infection as part of a states set in a Markov chain model, (states are susceptible, infected, asymptomatic, symptomatic, severe symptoms, critical, deceased and recovered), considering the probabilities of transiting from a certain state to another (for example, the probability of being infected, probability of recovering from disease, etc.) and also includes a graph to show the possible ways in course of disease. The data from Mexico on date June 10th, 2020 was used to build up the presented model. This works includes a graphic where is shown the contagion behavior of an infected person (symptomatic and asymptomatic) over susceptible people, this graphic material of the model was developed with Python tools, for better representing of graphics and visual information.

Keywords: states space, probability matrix, model graph, transition probabilities.

1. INTRODUCTION

The COVID-19 pandemic has spread around the world causing several problems (not only about health) over most of countries, which are trying to understand the disease with the

aim of establishing appropriate strategies to mitigate the disease meanwhile a vaccine and/or effective treatments are available.

Several models have been proposed around the world, using different tools and data from many countries. In [1] the authors use a Markov chains to describe a simple infected – recovered - dead model to predict the estimation of the total number of infected (cases) in some countries. Moreover, in [2] the SEIR (Susceptible-Exposed-Infective-Recovered) epidemiological model is mapped to a Markov chain to try to demonstrate the effectiveness of quarantine and isolation measures. Finally, in [3] a complex Markov chain is used to model the transmission mechanism of COVID-19 and the possible behavior of the disease when measurements like quarantine are inserted.

These models use some data for obtaining expected results but do not use complete data to show a scenario for the disease. In this work data made available from the official government is used [4] to construct a complete Markov chain model for the better understanding of the disease and its behavior in a specific country (Mexico).

Markov chains can be applied for epidemics because all of them are composed of several states, mainly three states: susceptible, infected, and recovered individuals, which can be represented as members of the discrete state space of a Markov model. An individual can go through the states of the epidemic defined by a determined probability (for example, the probability of being infected, and the probability of evolving into a critical state once the disease is caught). The transitions from one state to the other can be represented by a graph, also the probability values for representing the transition from one state to the any other can be calculated.

The simulation uses data from June 10th, 2020 because on June 1st, 2020 the government of Mexico announced the end of quarantine and allowed people to return gradually to their previous activities, following diverse recommendations, referred to as the new normality. Also, on that date the COVID-19 pandemic in Mexico had already reached its third month in duration, so with this time there was enough data to start the model.

2. LITERATURE REVIEW

2.1. Nonlinear Markov Chain Modelling of the Novel Coronavirus (Covid-19) Pandemic.

One of the three models reviewed is the one named Nonlinear Markov Chain Modelling of the Novel Coronavirus [1]. In this work a nonlinear Markov chains model is proposed to analyze and to understand the behavior of the Covid-19 pandemic. Data from China was used to build up that model. Thereafter, the nonlinear Markov chain model is employed to estimate the daily new Covid-19 cases in some countries including Italy, Spain, France, UK, the USA, Germany, Turkey, and Kuwait. The nonlinear Markov chain model can be expressed as:

$$S_{t+1} = (S_t + S_0) P \quad (1)$$

where S_{t+1} is the next state probability distribution, S_t is the current state probability distribution, S_0 is the new infected distribution, and $P = P(t, S_t)$ is the Markovian transition matrix. This model predicted that the Covid-19 pandemic would reach its peak in the first half of April 2020. Finally, the model estimated that the Covid-19 pandemic would be over before the first week of May 2020.

According to the results, the proposed model can efficiently capture the general behavior of the Covid-19 pandemic dispersion. All the reported data including the daily number of new Covid-19 cases, the daily number of deaths, the number of the daily Covid-19 tests are all assumed as correct.

2.2. Estimation of the Transmission Risk of the 2019-nCoV and Its Implication for Public Health Interventions

A deterministic compartmental model [2] was devised based on the clinical progression of the disease, epidemiological status of the individuals, and intervention measures. Sensitivity analyses show that interventions, such as intensive contact tracing followed by quarantine and isolation, can effectively reduce the control reproduction number and transmission risk.

The model in [2] uses data of laboratory-confirmed 2019-nCoV (the novel coronavirus) cases which occurred in mainland China from the WHO (World Health Organization) situation report.

A general SEIR-type epidemiological model was used, which incorporates appropriate compartments relevant to interventions such as quarantine, isolation, and treatment. The population was stratified as susceptible, exposed, infectious but not yet symptomatic, infectious with symptoms, hospitalized and recovered compartments, and further the work stratified the population to include quarantined susceptible, isolated exposed and isolated infected compartments.

In more detail, the analysis shows that increasing quarantine rate by 10 or 20 times will bring forward the peak by 6.5 or 9 days, and lead to a reduction of the peak value in terms of the number of infected individuals by 87% or 93%. This indicates that enhancing quarantine and isolation following contact

tracing and reducing the contact rate can significantly lower the peak and reduce the cumulative number of predicted reported cases.

2.3. Prediction of the COVID-19 outbreak based on a realistic stochastic model

In paper [3], a novel stochastic model is proposed which aims to account for the unique transmission dynamics of COVID-19 and capture the effects of intervention measures implemented in Mainland China.

Data used in that study include the numbers of confirmed diagnosis, recoveries and fatalities in the following provinces and cities of China: Beijing, Shanghai, Chongqing, Guangdong, Zhejiang and Hunan.

The proposed stochastic model aims to study the COVID-19 outbreak in the following aspects:

- Estimation of key epidemiology parameters
- Prediction of epidemic development
- Estimation of un-observable carriers and epidemic containment
- Assessment of control measures

The developed stochastic model has states like susceptible, exposed, quarantined, infected, asymptomatic, symptomatic, infected under hospitalization, recovered and dead.

Probability transitions of this model were structured based on Poisson rates and follow the way between infection, quarantine, symptom onset, hospitalization, symptom relief, recovery or death depending on the case.

In comparison with some existing models on COVID-19, the model features the employment of a stochastic dynamic as well as a comprehensive account for the infectious incubation period, the asymptomatic virus carriers, and the medical tracking measure with time latency, which make it probably closer to reality in these aspects. Moreover, the proposed model also sets the basis for further studies with individual/network-based models, which may not have an exact mean-field counterpart.

3. MATHEMATICAL FOUNDATIONS

Markov chains were first introduced in 1906 by Andrey Markov, with the goal of showing that the law of large numbers can apply to random variables that are not independent. In this process, the outcome of a given experiment can affect the outcome of the next experiment. This type of process is called a Markov chain.

Stochastic and Markovian modelling are of importance to many areas of science including physics, biology, engineering, as well as economics, finance, and social sciences. Also, it can be applied on epidemics, like the actual COVID-19.

As described in [5], for Markov Chains, it is considered a discrete-time stochastic process (Z_n) ; $n \in \mathbb{N}$ taking values in a discrete state space S , typically $S = Z$ (specifically, it is assumed that $S = \{1, 2, \dots, m\}$, for some positive integer m). The

S-valued process $(Z_n) n \in \mathbb{N}$ is said to be Markov, or to have the Markov property if, for all $n > 1$, the probability distribution of Z_{n+1} is determined by the state Z_n of the process at time n , and also does not depend on the past values of Z_k for $k = 0, 1, \dots, n - 1$.

In other words, for all $n > 1$ and all $i_0, i_1, \dots, i_n, j \in S$ is defined as:

$$P(Z_{n+1} = j | Z_n = i_n, Z_{n-1} = i_{n-1}, \dots, Z_0 = i_0) = P(Z_{n+1} = j | Z_n = i_n) \dots (2)$$

A Markov chain model is specified by identifying:

- ✓ The set of states “S”
- ✓ The set of possible transitions, namely, those pairs (i, j) for which $p_{i,j} > 0$
- ✓ The numerical values of those $p_{i,j}$ that are positive

The transition probabilities $p_{i,j}$ must be nonnegative, and sum to one:

$$\sum_{j=1}^m p_{i,j} = 1 \text{ for all } i \in S \quad (3)$$

All elements of a Markov chain model can be encoded in a transition probability matrix P , whose (i, j) entry is the probability of going from state i to state j in one step of the chain.

$$P = \begin{bmatrix} p_{1,1} & \dots & p_{1,m} \\ \vdots & \ddots & \vdots \\ p_{m,1} & \dots & p_{m,m} \end{bmatrix} \quad (4)$$

It is also helpful to lay out the model in the so-called transition probability graph, whose nodes are the states and whose arcs are the possible transitions as shown in Figure 1.

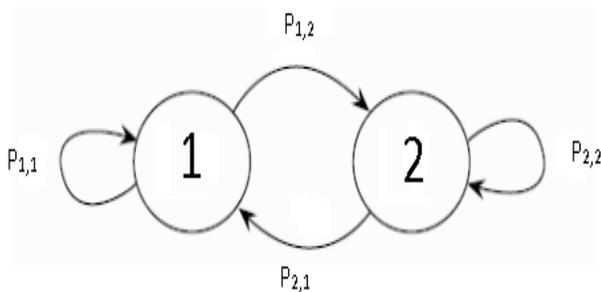


Fig. 1. Example of Markov Chain graph.

4. MATERIALS AND METHOD

4.1. States of the model

This section starts by explaining some concepts about the COVID-19 pandemic [6]. It is a highly contagious disease caused by the virus SARS-CoV-2, isolated for the first time in Wuhan, China. Once infected [7], an individual can show

symptoms or staying asymptomatic. Once an individual shows symptom, these may evolve into a critical case (severe symptoms like fever and/or difficult to breathe). If an individual does not resist the disease, unfortunately she/he dies. Critical and symptomatic people can get recovered from the disease and get immunity.

It is assumed that the population size is equal to n , and that the time is discrete (days). The phases of the epidemic can be represented as the set of states of a Markov Chain model, the states considered in this approach are described below:

Susceptible people. People who have never had the disease, so they are in risk of being infected.

Infected people. People who has caught the disease, in other words, people who are in latency period (incubation of the virus).

Asymptomatic people. People who has the disease, but do not show any symptom.

Symptomatic people. People who has the disease and show low symptoms.

Severe symptomatic people. People who has severe symptoms (difficult to breathe or high fever) and stay in hospitals.

Critical symptomatic people. People who is in intensive care.

Deceased people. People who has died.

Recovered people. People who has recovered from disease, and most of cases, get immunity.

4.2. Probabilities of the model

The probabilities for transiting from one state to another are explained below:

P (Su, I). Probability of being infected (go from Susceptible “Su” to Infected “I”)

P (I, A). Probability of being asymptomatic (go from Infected “I” to Asymptomatic “A”)

P (A, R). Probability of recovering from disease given that the person was asymptomatic (go from Asymptomatic “A” to Recovered “R”)

P (I, S). Probability of presenting symptoms (go from Infected “I” to Symptomatic “S”)

P (S, R). Probability of recovering from disease given that the person was symptomatic (go from Symptomatic “S” to Recovered “R”)

P (S, H). Probability of being hospitalized (go from Symptomatic “S” to Hospitalized “H”)

P (H, IC). Probability of requiring intensive care (go from Hospitalized “H” to Intensive Care “IC”)

P (H, R). Probability of recovering from disease given that the person was hospitalized (go from Hospitalized “H” to Recovered “R”)

P (IC, D). Probability of being dying by disease (go from Intensive Care “IC” to Dead “D”)

P (IC, R). Probability of recovering from disease given that the person was in intensive care (go from Intensive Care “IC” to Recovered “R”)

P (R, Su). Probability of being re - infected (go from Recovered “R” to Susceptible “Su”)

4.3. Graph for model

With the information above, a Markov Chain model graph is constructed as shown in Figure 2.

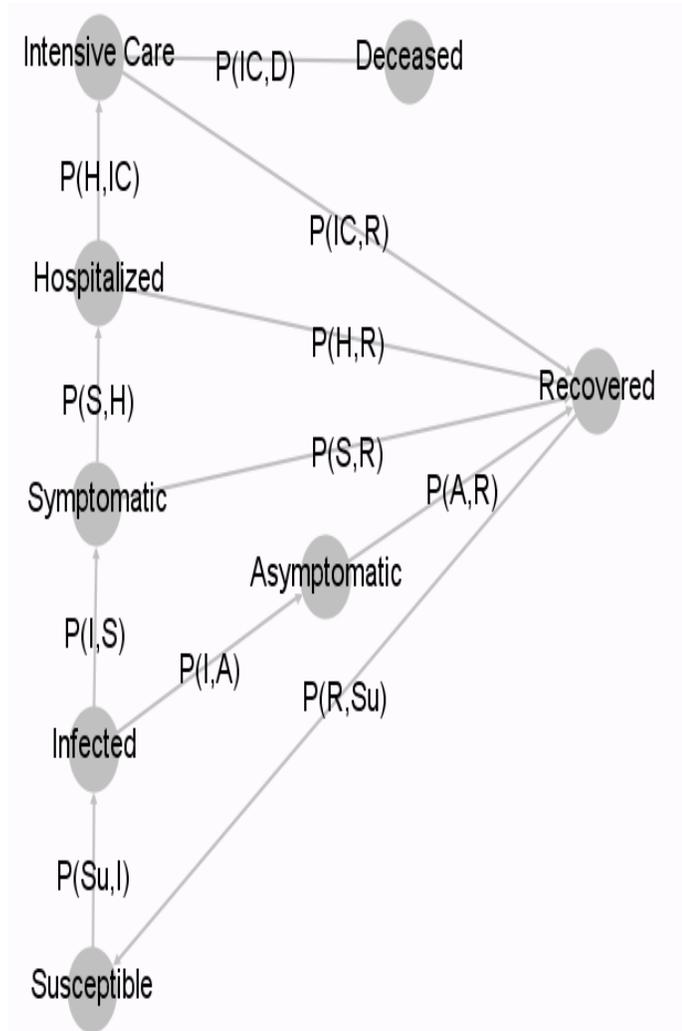


Fig. 2. Proposed graph for COVID-19 pandemic.

4.4. Transition probabilities matrix

The probability's matrix from the resulting probability graph is shown below:

$$\begin{bmatrix}
 1 - P(Su, I) & P(Su, I) & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
 0 & 0 & P(I, A) & P(I, S) & 0 & 0 & 0 & 0 & P(A, R) \\
 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & P(S, R) \\
 0 & 0 & 0 & 0 & P(S, H) & 0 & 0 & 0 & P(H, R) \\
 0 & 0 & 0 & 0 & 0 & P(H, IC) & 0 & 0 & P(IC, R) \\
 0 & 0 & 0 & 0 & 0 & 0 & P(IC, D) & 0 & 0 \\
 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
 P(R, Su) & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 - P(R, Su)
 \end{bmatrix} \dots(5)$$

5. RESULTS AND DISCUSSION

The model is constructed now. As described in [8], an individual can begin with symptoms in 3 days. If the individual is asymptomatic, it will be infectious for two weeks (14 days). It is not known the number of asymptomatic people, but it will be probably bigger than the number of people with symptoms. So, for practical data, it is considered that asymptomatic individuals are 1.5 more than symptomatic individuals.

For probability calculations, the next formulas are considered:
P (Su, I). Probability of being infected. It is calculated by the formula proposed in [8]:

$$1 - \left(1 - \frac{q_I y_I + q_A y_A}{n - y_H - y_{IC} - y_D - 1}\right)^N \quad (6)$$

where:

q_I and q_A are assumptions on the quality of producing any significant effect of the individuals infected.

$y_I, y_A, y_H, y_{IC}, y_D$, are the number of symptomatic, asymptomatic, hospitalized, intensive care and dead individuals, respectively.

Value n is the susceptible population and N is the number of meeting people in a day.

For calculation, the numbers are:

$q_I = 0.2$ and $q_A = 0.05$ (That is, we are assuming that asymptomatic individuals are less infectious than individuals who have symptoms [8]).

$n = 128,855,326$ (Mexico's population)

$N = 14$ (average number of people that a person has contact with).

Based in [4], with data from June 10th for Mexico, the numbers for $y_I, y_A, y_H, y_{IC}, y_D$ are:

$y_I =$ Number of infected people = 19,897

$y_A =$ Number of asymptomatic people = 1.5 (19,897) = 29,845

$y_H =$ Hospitalized people (33% of infected) = 19,897 (0.33) = 6,566

$y_{IC} =$ Intensive care = 378

$y_D =$ Dead people = 15,357

Hence, the contagion probability is:

$$P(Su, I) = 1 - \left(1 - \frac{(0.5)(19897) + (0.05)(29845)}{128855326 - 6566 - 378 - 15357 - 1}\right)^{14} = 0.027 \dots(7)$$

P (I, A). Probability of being asymptomatic. This is calculated by the next formula:

$$P(I, A) = \frac{y_A}{y_I + y_A} = \frac{29895}{19897 + 29895} = 0.60 \quad (8)$$

P (A, R). Probability of recovering from disease given that the person was asymptomatic. It is 1 because asymptomatic people in practice do not have the disease.

P (I, S). Probability of presenting symptoms:

$$1 - P(I, A) = 1 - 0.60 = 0.40 \quad (9)$$

P (S, R). Probability of recovering from the disease given that the person was symptomatic:

$$P(S, R) = \frac{Y_S - Y_H}{Y_R} = \frac{19897 - 6566}{94733} = 0.14 \quad (10)$$

P (S, H). Probability of being hospitalized:

$$1 - P(S, R) = 1 - 0.14 = 0.86 \quad (11)$$

P (H, IC). Probability of requiring intensive care:

$$P(H, IC) = \frac{Y_{IC}}{Y_H} = \frac{378}{6566} = 0.05 \quad (12)$$

P (H, R). Probability of recovering from the disease given that the person was hospitalized:

$$1 - P(H, IC) = 1 - 0.05 = 0.95 \quad (13)$$

P (IC, D). Probability of dying by the disease:

$$P(IC, D) = \frac{Y_D}{Total\ cases} = \frac{15357}{129184} = 0.11 \quad (14)$$

P (IC, R). Probability of recovering from the disease given that the person was in intensive care:

$$1 - P(IC, D) = 1 - 0.11 = 0.89 \quad (15)$$

P (R, Su). Probability of being re-infected. From all the information that has been published every day, in the media, some of them talk about a re-infected people. The exact data is unknown, so it will be assumed that a 0.10 people is re-infected. Hence, the probability of getting immunity is 0.90. The complete probability transition matrix is:

$$\begin{bmatrix} 0.973 & 0.027 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.60 & 0.40 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0.86 & 0 & 0 & 0.14 \\ 0 & 0 & 0 & 0 & 0 & 0.05 & 0 & 0.95 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.11 & 0.89 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0.10 & 0 & 0 & 0 & 0 & 0 & 0 & 0.90 \end{bmatrix}$$

Finally, Fig. 3 is presented for visualizing the expected number of secondary cases R_0 produced by an infectious individual, this is important to understand the total number of infected people that can result from an infected one. The formula to represent this is as follows (proposed in [8]):

$$R_0 = (P(I, S) * r_I * q_I + P(I, A) * r_A * q_A)(N)$$

r_I and r_A are the time in days that a person has suffered the disease. The values are 3 and 14, respectively.

N is the number of accumulable infected people. For simulating the secondary cases, it will be considered a period of 14 days (top period given by asymptomatic people).

In the case of asymptomatic people, they spread the infection during the 14 days that they have the disease, because they do not present symptoms those people think that they are in good health. If a quarantine is applied, those individuals stay at home, so the result is the detention or minimization of the contagion chain from a certain individual.

The resulting graphic is presented in Fig. 3:

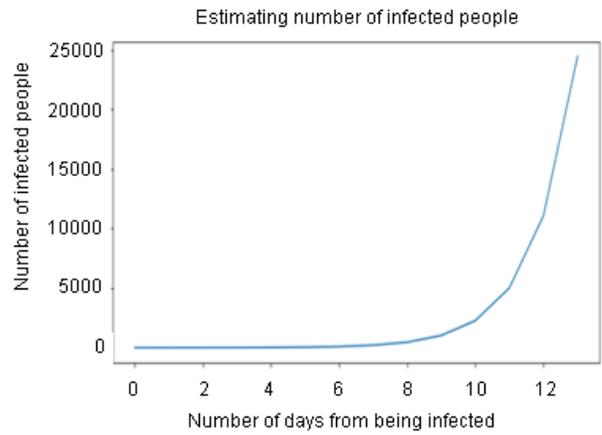


Fig. 3. Estimating infected people by an asymptomatic individual.

For symptomatic people, when an infected people starts presenting the symptoms of the disease, it will be in a period approximate between three to five days, in this graphic the minimum time of incubation period (three days) is used due that during this time the infected one does not know about having the disease. From here, the graphic shown in Fig. 4 is derived:

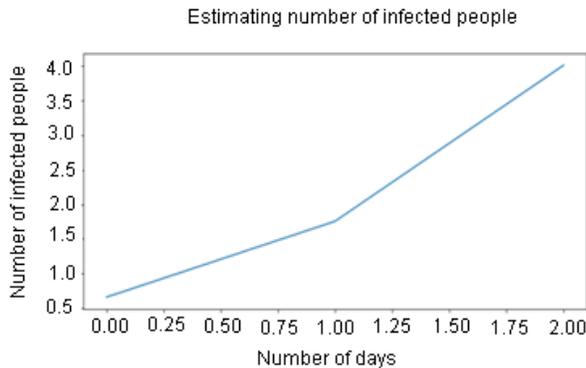


Fig. 4. Estimation of infected people by a symptomatic individual before presenting symptoms.

In the previous graphics, it is observed that an asymptomatic person can infect around 25000 people, this number represents the chains of contagion, that is, a person infects a certain number of people and those people infect others they meet, generating a large accumulation of infected people from a single infected individual. A symptomatic person can infect around four people before presenting symptoms (its period of being “asymptomatic” is from three to five days), if this person continues going out, she/he can infect a similar number like an asymptomatic person.

6. CONCLUSIONS

Markov chains model is a very useful tool for representing many phenomena in nature, epidemics are one of them. The states of disease (infected, symptomatic, asymptomatic, hospitalized, critical and deceased) were represented in a discrete Markov chain model with the respective probabilities, for analyzing the accurate behavior of the COVID-19 pandemic in Mexico.

This is a model with the following restrictions: it does not represent all the aspects of the pandemic (one of them is about the infection by touching contaminated objects). The exact number of asymptomatic people is difficult to know because these people do not know anything until a closer person (friends or family) has symptoms and the asymptomatic person is tested. About re-infected people, this is easier to know because these people have a previous positive result; when they get re-infected, they can tell the medics about the previous result. However, this is a general model for describing the main aspects of the pandemic.

In the graphics presented, it was observed that an asymptomatic people can spread the disease with a dangerous number (around 25000) while a symptomatic person before presenting symptoms can infect around four people, the principal concern

about these four people is that one of them can be asymptomatic and spread the disease dangerously.

Due to the previous observation, quarantine is a good way to stop the spread of the disease because asymptomatic people stay at home and this significantly reduces the number of infected people by reducing the contagion chain previously described.

For developing a more accurately model, it will be required some more information like the exact numbers of asymptomatic and re-infected people; for example, a good question is if people that have recovered from the disease and was not hospitalized, can be hospitalized given that have had the disease before?

If new information can be known about the pandemic, and more data is available, then the Markov chain model may generate more accurate results.

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